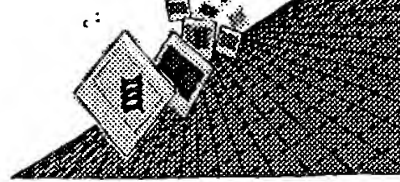


Sorbell

RAW SEQUENCE LISTING ERROR REPORT

BIOTECH. LOGY
SYSTEMS
BRANCH



#8/108
5/3/01

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/515,369

Source: 1633

Date Processed by STIC: 4/22/2001

RECEIVED

MAY - 1 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/515,369

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue. .
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of "Artificial" Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
(NEW RULES) Valid response is Artificial Sequence.
- 12 Use of <220>Feature Sequence(s) 2-13 are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
 Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/515,369

DATE: 04/22/2001
TIME: 14:17:03

Input Set : A:\56778.txt
Output Set: N:\CRF3\04222001\I515369.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Fisher, Paul
4 Madireddi, Malavi
6 <120> TITLE OF INVENTION: MELANOMA DIFFERENTIATION ASSOCIATED GENE-7 PROMOTER AND USES THEREOF
8 <130> FILE REFERENCE: 0575/56778/JPW/APE
10 <140> CURRENT APPLICATION NUMBER: 09/515,369
11 <141> CURRENT FILING DATE: 2000-02-29
13 <160> NUMBER OF SEQ ID NOS: 13
15 <170> SOFTWARE: PatentIn version 3.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 2286
19 <212> TYPE: DNA
20 <213> ORGANISM: Human
22 <400> SEQUENCE: 1
23 taatacgact cactataggg cgtcgactcg atcacctttt gaaccaggt ctgcctgcct 60
25 ccaaagcttg tactcataac tagattctca actgatgttg ggccaagggt cctaggttct 120
27 ctcttgacc ttcttctga agtaataatg ctatgataag ctcatcgag gctgaggccc 180
29 aggcacatgt ttgcctgaac tatccatgtt atatgattcc ttctcagac agagtgaagt 240
31 actcacgac ccagggtgac cctgaggcca gccaaagggt atccatgacc tcatgcctct 300
33 gttccagcct gccctttaac agctcatccc acctgcctgc cctccccgcc tatctgcaga 360
35 cagtagtcta ggatttcagc tgccctgggg gctcattttc cctctcagct tctgtcttta 420
37 gctgtctctt gctctccact cacctattac tccagcactc tcacctggtc ttcttttctg 480
39 tctcatcact gcctcttgac atctttatct catagtagtt agttaggggt tcttggtaat 540
41 gccctaaatc cacatggttg gaagggggga gtggggggaag agagtgcgt gtggggctgt 600
43 gcctacttct ggagggttaag actcggggccc tccaggaaca aaggattcag gctgggtggca 660
45 gctatagcca agcagactgc tggccaggga ttgcaaagga gtattttgtt tgcttaagaa 720
47 aataaacaac actgagtatg agatggaggg aggggggtgt ggtgccagag agattgggaa 780
49 gagtctgcca aggggtgtgt ctactcactc tctcttttct ttcatctcc actgagctgg 840
51 aggcagttat cctgtccccc acgtcacatt cctactcccg ttcccatgc ctggaccag 900
53 gttgggcaaa ctcttctgt aaagaaccag acaggaacta ttttaggtc tgtgtgcat 960
55 atggtctcag tcacaactac tcatctctgc ctctgtagca cgaaagcaat tagcaacaat 1020
57 atgtcaacaa acatatgtga ccccatgaaa actttattta ttatggatac ggaaacctga 1080
59 aaataatgtc tttcttttga ttttttcccc aatcattaaa aaacgtaaaa actactctta 1140
61 ggtcgcaagg ttaagccatt ctacagcttag cagtggcagg ctggatttgg cttgtgacct 1200
63 acagttggcc aatccctgat tccaaaatg ttttctcag ggatgtgggc aaatacttat 1260
65 ggggaagtgt ggattaaaca gatttaagaa gcatcagaca ttccaggac gggctagcac 1320
67 atgccagggc tctctaactg acctcatttg attcatctgt ttcatggagg atcttgcaag 1380
69 acaagaattc ctcaaaccta gactctgagg actgtgcttt gggaaacact gctctgcttg 1440
71 atgccctcac tgggcacatg gtagaatcta gagctgagt ccttgctagc tggagatagg 1500
73 gtcagagctc ttgactgccc tggcagctct gacacatcac gctgtctgtg tccctgagt 1560
75 ggttcagagc cacacaggcc aagactagcc caccagagca ccaggcctcc cagctttctg 1620
77 ggettggtcca tgcgtacatt tcttattct tcttggttcc cagaacctaa ggagaggcac 1680
79 attttggttg agtgattata accctaggga ccatgggtag ctgcatgtca ggaaacactc 1740
81 ctcaacttcc tggccctgat ggattaaagg agaggtaact acaggttatt tcttcgctgt 1800
83 ggaactactgt cccagcatga ataggcatc attattgaat tattttgaca ggaaggagac 1860
85 tgggtgatgc tgcacagtaa taatgtattt acatgtgtac agagtttacc aagcacctct 1920
87 gtgtgtgttt tgccttggtt tattacactt gggacaaatt tttaaaattt atacatgcag 1980
89 agactgcagc gcagagaagc taagagactt gccctgccc acacagccag tggtagagcc 2040

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/515,369

DATE: 04/22/2001
 TIME: 14:17:03

Input Set : A:\56778.txt
 Output Set: N:\CRF3\04222001\I515369.raw

91 tgaactcaaa cccaggtctc atctcacctc aggggctgct ttcccatcg ctgtattgtc 2100
 93 cttaaagtga tgggtgacta ggcaatgaag taattctcta ggaaagcatg accaatttcc 2160
 95 cttctccac ctcctctttt ttctccacc cctccccat cagccccc atatatgcc 2220
 97 aaatctccac aaagcettgc ttgctgcaa acctttactt ctgaaatgac ttccacggct 2280
 99 gggacg 2286

102 <210> SEQ ID NO: 2
 103 <211> LENGTH: 21
 104 <212> TYPE: DNA

C--> 105 <213> ORGANISM: Artificial
 W--> 107 <220> FEATURE:
 W--> 107 <223> OTHER INFORMATION:
 107 <400> SEQUENCE: 2
 108 cgtcccagcc gtggaagtca t 21
 111 <210> SEQ ID NO: 3
 112 <211> LENGTH: 21
 113 <212> TYPE: DNA

C--> 114 <213> ORGANISM: Artificial
 W--> 116 <220> FEATURE:
 W--> 116 <223> OTHER INFORMATION:
 116 <400> SEQUENCE: 3
 117 aggctggatt tggttgtga c 21
 120 <210> SEQ ID NO: 4
 121 <211> LENGTH: 21
 122 <212> TYPE: DNA

C--> 123 <213> ORGANISM: Artificial
 W--> 125 <220> FEATURE:
 W--> 125 <223> OTHER INFORMATION:
 125 <400> SEQUENCE: 4
 126 ctgtttaatc cagcacttcc c 21
 129 <210> SEQ ID NO: 5
 130 <211> LENGTH: 21
 131 <212> TYPE: DNA

C--> 132 <213> ORGANISM: Artificial
 W--> 134 <220> FEATURE:
 W--> 134 <223> OTHER INFORMATION:
 134 <400> SEQUENCE: 5
 135 cgttgatga ctcagccgga a 21
 138 <210> SEQ ID NO: 6
 139 <211> LENGTH: 20
 140 <212> TYPE: DNA

C--> 141 <213> ORGANISM: Artificial
 W--> 143 <220> FEATURE:
 W--> 143 <223> OTHER INFORMATION:
 143 <400> SEQUENCE: 6
 144 tgcagattgc gcaatctgca 20
 147 <210> SEQ ID NO: 7
 148 <211> LENGTH: 21
 149 <212> TYPE: DNA

C--> 150 <213> ORGANISM: Artificial

(global errors)

see item 11 on Error Summary Sheet
 see item 12 on Error Summary Sheet

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/515,369

DATE: 04/22/2001
TIME: 14:17:03

Input Set : A:\56778.txt
Output Set: N:\CRF3\04222001\I515369.raw

```

W--> 152 <220> FEATURE:
W--> 152 <223> OTHER INFORMATION:
152 <400> SEQUENCE: 7
153 cgcttgatga cttggccgga a 21
156 <210> SEQ ID NO: 8
157 <211> LENGTH: 22
158 <212> TYPE: DNA
C--> 159 <213> ORGANISM: Artificial
W--> 161 <220> FEATURE:
W--> 161 <223> OTHER INFORMATION:
161 <400> SEQUENCE: 8
162 tgcagagaga ctagtctctg ca 22
165 <210> SEQ ID NO: 9
166 <211> LENGTH: 61
167 <212> TYPE: DNA
C--> 168 <213> ORGANISM: Artificial
W--> 170 <220> FEATURE:
W--> 170 <223> OTHER INFORMATION:
170 <400> SEQUENCE: 9
171 uuguauuuau uacaacucua uuuaauuuau gucaguauuu caacugaagu ucuauuuauu 60
173 u 61
176 <210> SEQ ID NO: 10
177 <211> LENGTH: 15
178 <212> TYPE: DNA
C--> 179 <213> ORGANISM: Artificial
W--> 181 <220> FEATURE:
W--> 181 <223> OTHER INFORMATION:
181 <400> SEQUENCE: 10
182 uauuuauuuu uuuaa 15
185 <210> SEQ ID NO: 11
186 <211> LENGTH: 51
187 <212> TYPE: DNA
C--> 188 <213> ORGANISM: Artificial
W--> 190 <220> FEATURE:
W--> 190 <223> OTHER INFORMATION:
190 <400> SEQUENCE: 11
191 uauuuuuuuu auuuuuuuuu uuuuuuuuuu uuuuuuuuuu uuuuuuuuuu a 51
194 <210> SEQ ID NO: 12
195 <211> LENGTH: 34
196 <212> TYPE: DNA
C--> 197 <213> ORGANISM: Artificial
W--> 199 <220> FEATURE:
W--> 199 <223> OTHER INFORMATION:
199 <400> SEQUENCE: 12
200 auuuuuuuuu auuuuuuuuu uuuuuuuuuu uuua 34
203 <210> SEQ ID NO: 13
204 <211> LENGTH: 56
205 <212> TYPE: DNA
C--> 206 <213> ORGANISM: Artificial

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RAW SEQUENCE LISTING DATE: 04/22/2001
PATENT APPLICATION: US/09/515,369 TIME: 14:17:03

Input Set : A:\56778.txt
Output Set: N:\CRF3\04222001\I515369.raw

W--> 208 <220> FEATURE:

W--> 208 <223> OTHER INFORMATION:

208 <400> SEQUENCE: 13

209 guuuuuuuuu uuuuuuuuuu gauggauucu cagauuuuuu uuuuuuuuuu uuauuu 56

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/515,369

DATE: 04/22/2001

TIME: 14:17:04

Input Set : A:\56778.txt

Output Set: N:\CRF3\04222001\I515369.raw

L:105 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:107 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:107 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:114 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:116 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:116 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:123 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:125 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:125 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:132 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:134 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:134 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:141 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:143 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:143 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:150 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:152 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:152 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:159 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:161 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:161 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:168 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:170 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:170 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:179 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:181 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:181 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:188 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:190 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:190 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:197 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:199 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:199 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:206 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:208 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:208 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: